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=> s hep(w) 27 or hep27
L1 24 HEP(W) 27 OR HEP27

=> s l1 and antibod?
L2 8 L1 AND ANTIBOD?

=> d 1-8 ti

L2 ANSWER 1 OF 8 MEDLINE
TI A human short-chain dehydrogenase/reductase gene: structure, chromosomal localization, tissue expression and subcellular localization of its product.

L2 ANSWER 2 OF 8 MEDLINE
TI Identification of peroxisomal proteins by using M13 phage protein VI phage display: molecular evidence that mammalian peroxisomes contain a 2,4-dienoyl-CoA reductase.

L2 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Construction and high cytoplasmic expression of a tumoricidal single-chain **antibody** against hepatocellular carcinoma.

L2 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI A human short-chain dehydrogenase/reductase gene: Structure, chromosomal localization, tissue expression and subcellular localization of its product.

L2 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Tumor suppressive monoclonal **antibody** belonging to the VH 7183 family directed to the oncodevelopmental carbohydrate antigen on human hepatocellular carcinoma.

L2 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2003 ACS
TI Construction and high cytoplasmic expression of a tumoricidal single-chain **antibody** against hepatocellular carcinoma

L2 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2003 ACS
TI Tumor suppressive monoclonal **antibody** belonging to the VH 7183 family directed to the oncodevelopmental carbohydrate antigen on human hepatocellular carcinoma

L2 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS
TI Nucleic acids encoding human short-chain alcohol dehydrogenase-related molecules ScRM-1 and ScRM-2

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 5 DUP REM L2 (3 DUPLICATES REMOVED)

=> d 1-5 ti

L3 ANSWER 1 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
TI Tumor suppressive monoclonal **antibody** belonging to the VH 7183 family directed to the oncodevelopmental carbohydrate antigen on human hepatocellular carcinoma.

L3 ANSWER 2 OF 5 MEDLINE DUPLICATE 2
TI A human short-chain dehydrogenase/reductase gene: structure, chromosomal localization, tissue expression and subcellular localization of its product.

L3 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
TI Construction and high cytoplasmic expression of a tumoricidal single-chain **antibody** against hepatocellular carcinoma.

L3 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2003 ACS
TI Nucleic acids encoding human short-chain alcohol dehydrogenase-related molecules ScRM-1 and ScRM-2

L3 ANSWER 5 OF 5 MEDLINE
TI Identification of peroxisomal proteins by using M13 phage protein VI phage display: molecular evidence that mammalian peroxisomes contain a 2,4-dienoyl-CoA reductase.

=> d 1-5 bib ab

L3 ANSWER 1 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 2002:327468 BIOSIS
DN PREV200200327468
TI Tumor suppressive monoclonal **antibody** belonging to the VH 7183 family directed to the oncodevelopmental carbohydrate antigen on human hepatocellular carcinoma.
AU Sandee, Duanpen; Tungpradabkul, Sumalee; Laohathai, Kingkarn; Punyammalee, Boonnum; Kohda, Katsunori; Takagi, Masahiro; Imanaka, Tadayuki (1)
CS (1) Department of Synthetic Chemistry and Biological Chemistry, Graduate School of Engineering, Kyoto University, Sakyo-ku, Kyoto, 606-8501: imanaka@sbchem.kyoto-u.ac.jp Japan
SO Journal of Bioscience and Bioengineering, (2002) Vol. 93, No. 3, pp. 266-273. http://www.elsevier.com/locate/jfermbio. print. ISSN: 1389-1723.
DT Article
LA English
AB **Hep27** monoclonal **antibody** (**Hep27** Mab) was raised by immunizing BALB/c mice with cells of the Thai human hepatocellular carcinoma (HCC) cell line HCC-S102 using hybridoma technology. The **Hep27** Mab recognizes oncofetal development antigens by reacting with many HCC, other cancers, fetal and newborn liver but not adult liver. The **Hep27** Mab alone markedly inhibits the growth of hepatocellular carcinoma cell lines (65% viability on the third day), suggesting its clinical usefulness. Moreover, complementary DNA (cDNA) for active variable regions of both heavy and light chains of the **antibody** has been cloned. Sequence analysis of the variable region of the **Hep27** Mab revealed that the VH and VL genes belong to the VH 7183 and VK families, respectively. We have also characterized the

reactivity of the **Hep27** Mab to synthetic carbohydrate epitopes and 1-phenyl-2-decanoylamino-3-morpholino-1-propanol (PDMP)-treated HCC-S102 cells. The results showed that the **Hep27** Mab recognizes a neoglycolipid containing a mucin core unit and PDMP treatment reduced **Hep27** Mab binding activity to HCC-S102 cells, indicating that the **Hep27** Mab recognizes a glycolipid antigen on HCC-S102 cells. This Mab may be potentially useful for studying antigenic expression in hepatocellular carcinoma and as a targeting agent for radioimmunodetection and immunoconjugated therapy.

L3 ANSWER 2 OF 5 MEDLINE DUPLICATE 2
AN 2002257498 MEDLINE
DN 21992428 PubMed ID: 11997086
TI A human short-chain dehydrogenase/reductase gene: structure, chromosomal localization, tissue expression and subcellular localization of its product.
AU Pellegrini Silvia; Censini Stefano; Guidotti Silvia; Iacopetti Paola; Rocchi Mariano; Bianchi Marco; Covacci Antonello; Gabrielli Franco
CS Department of Experimental Pathology and Medical Biotechnology, University of Pisa, Via S. Zeno 37, I-56127 Pisa, Italy.
SO BIOCHIMICA ET BIOPHYSICA ACTA, (2002 Apr 12) 1574 (3) 215-22. Journal code: 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF244132
EM 200208
ED Entered STN: 20020509
Last Updated on STN: 20020807
Entered Medline: 20020806
AB We have previously described the cloning of **Hep27**, a short-chain dehydrogenase/reductase, which is synthesized in human hepatoblastoma HepG2 cells following growth arrest induced by butyrate treatment. The present report describes the cloning, the structure and the physical and cytogenetic mapping of the gene coding for **Hep27**. We also show that **Hep27** is synthesized in a limited number of human normal tissues and that it is localized in the nuclei and cytoplasm of HepG2 cells.

L3 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
AN 2002:564062 BIOSIS
DN PREV200200564062
TI Construction and high cytoplasmic expression of a tumoricidal single-chain **antibody** against hepatocellular carcinoma.
AU Sandee, Duanpen; Tungpradabkul, Sumalee; Tsukio, Manae; Imanaka, Tadayuki; Takagi, Masahiro (1)
CS (1) School of Materials Science, Japan Advanced Institute of Science and Technology, Ishikawa, 923-1292: duanpensandee@hotmail.com, scstp@mahidol.ac.th, manae-yamaguchi@aist.go.jp, imanaka@sbchem.kyoto-u.ac.jp, takagi@jaist.ac.jp Japan
SO BMC Biotechnology, (September 12, 2002) Vol. 2, No. 16 Cited October 7, 2002, pp. No Pagination. http://www.biomedcentral.com/1472-6750. online. ISSN: 1472-6750.
DT Article
LA English
AB Background: **Hep27** monoclonal (**Hep27** Mab) is an **antibody** against hepatocellular carcinoma. **Hep27** Mab itself can inhibit the growth of a hepatocellular carcinoma cell line (HCC-S102). We attempted to produce a single-chain fragment (scFv), a small fragment containing an antigen-binding site of **Hep27** Mab, by using DNA-recombinant techniques. Results: The sequences encoding the

variable regions of heavy (VH) and light (VL) chains of a murine **Hep27** Mab were linked together by a linker peptide (Gly4Ser)3 and tagged with a hexahistidine at the C-terminal; the resultant DNA construct was expressed in E. coli as an insoluble protein. The denatured scFv was refolded and purified by immobilized metal ion affinity chromatography (12 mg/l with a molecular weight of 27 kDa). Hep27scFv exhibited a tumoricidal activity against the HCC-S102 cell as its parental **antibody** (**Hep27** Mab). Conclusion: This scFv may be a potential candidate for a targeting agent in HCC immunodiagnosis or immunotherapy.

L3 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2003 ACS
AN 2000:68545 CAPLUS
DN 132:103778
TI Nucleic acids encoding human short-chain alcohol dehydrogenase-related molecules ScRM-1 and ScRM-2
IN Bandman, Olga; Tang, Y. Tom; Corley, Neil C.; Azimzai, Yalda; Baughn, Mariah R.
PA Incyte Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000004135	A2	20000127	WO 1999-US16164	19990716
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
	RW: AT, BE, BF, BJ, CF, CG, CH, CM, CY, DE, SN, TD, TG, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG				
	CA 2333471	AA	20000127	CA 1999-2333471	19990716
	AU 9950017	A1	20000207	AU 1999-50017	19990716
	EP 1097219	A2	20010509	EP 1999-934112	19990716
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, FI, RO				
	JP 2002520046	T2	20020709	JP 2000-560233	19990716
PRAI	US 1998-116750	A	19980716		
	US 1998-160074P	P	19980716		
	WO 1999-US16164	W	19990716		

AB The invention provides a human short-chain alc. dehydrogenase (SCAD)-related mols. (ScRM) and polynucleotides which identify and encode ScRM. Nucleic acids encoding ScRM-1 and ScRM-2 were first identified in Incyte clones 1240869 and 2060002 from lung and ovarian cDNA libraries, resp., using a computer search for amino acid sequence alignments; consensus sequences were derived from overlapping and/or extended nucleic acid sequences. ScRM-1 is 278 amino acids in length, has structural homol. with human **Hep27**, and is expressed in various libraries, .gtoreq.67% of which ar e proliferative and .gtoreq.34% of which involve immune response. ScRM-2 is 564 amino acids in length, has structural homol. with Caenorhabditis elegans alc. dehydrogenase/ribitol dehydrogenase, and is expressed in various libraries, .gtoreq.65% of which are proliferative and .gtoreq.24% of which involve immune response. The invention also provides expression vectors, host cells, **antibodies** , agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders assocd. with expression of ScRM.

L3 ANSWER 5 OF 5 MEDLINE
AN 1999267333 MEDLINE

DN 99267333 PubMed ID: 10333503
TI Identification of peroxisomal proteins by using M13 phage protein VI phage display: molecular evidence that mammalian peroxisomes contain a 2,4-dienoyl-CoA reductase.
AU Fransen M; Van Veldhoven P P; Subramani S
CS Department of Biology, University of California at San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0322, USA.
NC DK41737 (NIDDK)
SO BIOCHEMICAL JOURNAL, (1999 Jun 1) 340 (Pt 2) 561-8.
Journal code: 2984726R. ISSN: 0264-6021.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF044574
EM 199907
ED Entered STN: 19990806
Last Updated on STN: 19990806
Entered Medline: 19990729
AB To elucidate unknown mammalian peroxisomal enzymes and functions, we subjected M13 phage expressing fusions between the gene encoding protein VI and a rat liver cDNA library to an immunoaffinity selection process in vitro (biopanning) with the use of **antibodies** raised against peroxisomal subfractions. In an initial series of biopanning experiments, four different cDNA clones were obtained. These cDNA species encoded two previously identified peroxisomal enzymes, catalase and urate oxidase, and two novel proteins that contained a C-terminal peroxisomal targeting signal (PTS1). A primary structure analysis of these novel proteins revealed that one, ending in the tripeptide AKL, is homologous to the yeast peroxisomal 2,4-dienoyl-CoA reductase (EC 1.3.1.34; DCR), an enzyme required for the degradation of unsaturated fatty acids, and that the other, ending in the tripeptide SRL, is a putative member of the short-chain dehydrogenase/reductase (SDR) family, with three isoforms. Green fluorescent protein (GFP) fusions encoding GFP-DCR-AKL, GFP-DCR, GFP-SDR-SRL and GFP-SDR were expressed in mammalian cells. The analysis of the subcellular location of the recombinant fusion proteins confirmed the peroxisomal localization of GFP-DCR-AKL and GFP-SDR-SRL, as well as the functionality of the PTS1. That the AKL protein is indeed an NADPH-dependent DCR was demonstrated by showing DCR activity of the bacterially expressed protein. These results demonstrate at the molecular level that mammalian peroxisomes do indeed contain a DCR. In addition, the results presented here indicate that the protein VI display system is suitable for the isolation of rare cDNA clones from cDNA libraries and that this technology facilitates the identification of novel peroxisomal proteins.

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:58:46 ON 01 MAY 2003
L1 24 S HEP(W) 27 OR HEP27
L2 8 S L1 AND ANTIBOD?
L3 5 DUP REM L2 (3 DUPLICATES REMOVED)

=> dup rem l1
PROCESSING COMPLETED FOR L1
L4 15 DUP REM L1 (9 DUPLICATES REMOVED)

=> s l4 not l3
L5 10 L4 NOT L3

=> d 1-10 bib ab

L5 ANSWER 1 OF 10 MEDLINE
AN 2002211498 MEDLINE
DN 21945271 PubMed ID: 11944995
TI Genomic organization of the human gene **HEP27**: alternative promoter usage in HepG2 cells and monocyte-derived dendritic cells.
AU Heinz Sven; Krause Stefan W; Gabrielli Franco; Wagner Harald M; Andreesen Reinhard; Rehli Michael
CS Department of Hematology and Oncology, University Hospital, 93042 Regensburg, Germany.
SO GENOMICS, (2002 Apr) 79 (4) 608-15.
Journal code: 8800135. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200208
ED Entered STN: 20020412
Last Updated on STN: 20020817
Entered Medline: 20020816
AB We used representational difference analysis to discover new genes with specific expression in dendritic cells. Among other genes, we identified **HEP27**, encoding a member of the short chain alcohol dehydrogenase/reductase family to be upregulated during monocyte to dendritic cell differentiation. Originally cloned from hepatocellular carcinoma cells (HepG2), **HEP27** was exclusively expressed in monocyte-derived dendritic cells within the hematopoietic system. The presence of different transcripts in monocyte-derived dendritic cells, HepG2 cells, and various tissues could be traced back to alternative splicing and alternative promoter usage. We describe here the complete genomic organization of **HEP27**, including two alternative promoter regions: a hepatocyte-specific promoter which was induced by the histone deacetylase inhibitor sodium butyrate in several other cell types, and a second upstream promoter which was specifically active in monocyte-derived dendritic cells. Its exclusive usage in monocyte-derived dendritic cells makes the alternative **HEP27** promoter an interesting target to study dendritic-cell-specific gene regulation.

L5 ANSWER 2 OF 10 MEDLINE
AN 96035881 MEDLINE
DN 96035881 PubMed ID: 7556196
TI A nuclear protein, synthesized in growth-arrested human hepatoblastoma cells, is a novel member of the short-chain alcohol dehydrogenase family.
AU Gabrielli F; Donadel G; Bensi G; Heguy A; Melli M
CS Department of Physiology and Biochemistry, University of Pisa, Italy.
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1995 Sep 1) 232 (2) 473-7.
Journal code: 0107600. ISSN: 0014-2956.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U31875
EM 199511
ED Entered STN: 19951227
Last Updated on STN: 19970203
Entered Medline: 19951114
AB We have described a protein (**Hep27**) [Donadel, G., Garzelli, C., Frank, R. & Gabrielli, F. (1991) Eur. J. Biochem. 195, 723-729] which is synthesized and accumulated in the nucleus of human hepatoblastoma (HepG2) cells, following growth arrest induced by butyrate treatment. The

synthesis of **Hep27** is inhibited in cells that, released from the butyrate block, have resumed DNA synthesis. This report describes the cloning and the characterization of the cDNA coding for the **Hep27** protein. The translation of the **Hep27** cDNA predicts an amino acid sequence that can be aligned with those of the known short-chain alcohol dehydrogenase enzymes (SCAD) family. Both the recognition of enzymic functional domains and the similarity with the SCAD family of proteins of several amino acid blocks throughout the molecule, strongly suggest that this protein is a new member of the SCAD family. In agreement with its nuclear localization **Hep27** has a region similar to the bipartite nuclear-targeting sequence. The study of **Hep27** mRNA expression and protein synthesis suggests the existence of a regulation at the post-transcriptional level. The possible nuclear role of the **Hep27** protein is discussed.

L5 ANSWER 3 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:45910 BIOSIS
DN PREV200000045910
TI Immature dendritic cells are the major source of monocyte chemotactic protein 4 (MCP-4.
AU Wagner, Harald M. (1); Heinz, Sven (1); Krause, Stefan W. (1); Andreesen, Reinhard (1)
CS (1) Dept. of Hematology and Oncology, University of Regensburg, Regensburg Germany
SO Blood, (Nov. 15, 1999) Vol. 94, No. 10 SUPPL. 1 PART 1, pp. 210a. Meeting Info.: Forty-first Annual Meeting of the American Society of Hematology New Orleans, Louisiana, USA December 3-7, 1999 The American Society of Hematology
. ISSN: 0006-4971.
DT Conference
LA English

L5 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2002:531606 CAPLUS
DN 137:74482
TI Detection of genetic polymorphisms in drug-metabolizing enzyme genes and their use for evaluation and screening of drugs
IN Nakamura, Yusuke; Sekine, Akihiro; Iida, Aritoshi; Saito, Susumu
PA Riken Corp., Japan
SO PCT Int. Appl., 2858 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002052044	A2	20020704	WO 2001-XA11592	20011227
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002052044	A2	20020704	WO 2001-JP11592	20011227
WO 2002052044	A3	20030320		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,				

PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI JP 2000-399443 A 20001227
JP 2001-135256 A 20010502
JP 2001-256862 A 20010827
WO 2001-JP11592 A 20011227

AB The present invention relates to genetic polymorphism data, compns. and methods for detecting genetic polymorphisms, methods for evaluating drugs using genetic polymorphisms, and screening methods for drugs. Thus, 7669 sep. single nucleotide polymorphisms (SNP) are provided in human genes encoding drug-metabolizing enzymes. In some embodiments, a drug-metabolizing enzyme is at least one of the following: epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alc. dehydrogenase, esterase, NDUF, cytochrome P 450, and ATP-binding cassette. In one example, a correlation is demonstrated between optimal amts. of azathioprine (an immunosuppressive agent) and various combinations of the alleles at the 868th SNP of intron 3 of thiopurine S-methyltransferase gene (G or T alleles) and the 2682nd SNP of intron 3 (C or A alleles). [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L5 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2002:377658 CAPLUS
DN 136:397858
TI Real-time RT-PCR quantitative assay for detection of enzymes associated with phase I drug metabolism analysis
IN Nishimura, Masuhiro; Yaguchi, Hiroshi; Naito, Shinsaku; Hiraoka, Isao
PA Ohtsuka Pharmaceutical Co., Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 36 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2002142780	A2	20020521	JP 2001-257338	20010828
PRAI	JP 2000-267163	A	20000904		

AB A method and reagent kit contg. probe and primer pairs for real-time RT-PCR quantification of the enzymes, are disclosed. The probe is labeled with a pair of reporter chromophore and a quencher, which cause fluorescence resonance energy transfer (FRET). Use of a probe labeled at 5' end with FAM and at 3' end with TAMRA is described.

L5 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2002:200515 CAPLUS
DN 137:87995
TI Analysis of gene induction in human fibroblasts and bladder cancer cells exposed to the methylation inhibitor 5-Aza-2'-deoxycytidine
AU Liang, Gangning; Gonzales, Felicidad A.; Jones, Peter A.; Orntoft, Torben F.; Thykjaer, Thomas
CS USC/Norris Comprehensive Cancer Center, Department of Urology, Biochemistry and Molecular Biology, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA
SO Cancer Research (2002), 62(4), 961-966
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research

DT Journal
LA English
AB Hypermethylation of the promoters of cancer-related genes is often assocd. with their inactivation during tumorigenesis. Several preclin. and clin. trials have been developed to use DNA methylation inhibitors, such as 5-aza-2'-deoxycytidine (5-Aza-CdR) in attempts to reactivate silenced genes in human cancers. The authors used high-d. oligonucleotide gene expression microarrays to examine the effects of 5-Aza-CdR treatment on human fibroblast cells (LD419) and a human bladder tumor cell line (T24). Data obtained 8 days after recovery from 5-Aza-CdR treatment showed that more genes were induced in tumorigenic cells (61 genes induced; .gtoreq.4-fold) than nontumorigenic cells (34 genes induced; .gtoreq.4-fold). Approx. 60% of induced genes did not have CpG islands within their 5' regions, suggesting that some genes activated by 5-Aza-CdR may not result from the direct inhibition of promoter methylation. Interestingly, a high percentage of genes activated in both cell types belonged to the IFN signaling pathway, confirming data from other tumor cell types.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2002:123253 CAPLUS
DN 136:179834
TI Algorithm for identifying short chain dehydrogenases/reductases (SDR) using minimal core SDR motifs and a method for identifying pharmaceutical modulators for members of the SDR family
IN Wilckens, Thomas
PA Bionetworks G.m.b.H., Germany
SO PCT Int. Appl., 168 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002012544	A2	20020214	WO 2001-EP9140	20010807
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2001082077	A5	20020218	AU 2001-82077	20010807
PRAI	US 2000-223436P	P	20000807		
	WO 2001-EP9140	W	20010807		

AB The present invention relates to a method for identifying or verifying members of the short chain dehydrogenase (SDR) family, to a method for providing modulators for members of the SDR family, and to the prepn. of pharmaceutical agents using these modulators. An algorithm using core SDR motifs for searching members of the SDR family. The so-called SDR_Finder equipped with fuzzy logic is based on the implementation of functional data both on the three-dimensional structure and on the biol. function. Implementation is hierarchically structured according to the smallest common denominator having a functional meaning; SDR candidates are searched for those having a very low homol. or hardly conserved core motifs, enabling a considerably higher specificity. The algorithm allows for an assignment of target sequences to be an SDR sequence with a confidence level of >95%. Candidates identified in the public databases

are classified as human SDRs, mouse SDRs, bacterial SDRs, FabG proteins, and SDRs from fungi. Pharmaceuticals for immune regulation or autoimmunity treatment may be developed based on modulators for SDR candidates such as 17.beta.-hydroxy steroid dehydrogenase, AF0078850, TV5-1, **HEP-27**, UDP-glucose epimerase, SDR_SRL, AF067174, AF151840, AF151844, DKFZ_ORF, WWOX-ORF, and CR3.

L5 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2002:107579 CAPLUS
DN 136:162405
TI Tissue-associated proteins and their uses
IN Brown, Joseph P.; Pritchard, David; Demas, Vasiliki; Burmer, Glenna C.
PA Lifespan Biosciences, Inc., USA
SO PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DT Patent
LA English
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PI	WO 2002010428	A2	20020207	WO 2001-US24237	20010801
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2002107215	A1	20020808	US 2001-920302	20010731
PRAI	US 2000-222224P	P	20000801		

AB Provided are proteins and polynucleotides and methods for expressing them in specific healthy or diseased tissues. Also provided is a method of diagnosing cancer based on the protein or nucleotide expressed by the tissue in question. In another embodiment is a method to type healthy tissues based on the protein or nucleotide expressed by the tissue in question. Also provided is a method to deliver therapeutic agents to cancerous cells and to screen for antitumor agents based on the types of proteins expressed by healthy and cancerous cells.

L5 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2001:527300 CAPLUS
DN 136:227562
TI Catalog of 434 single-nucleotide polymorphisms (SNPs) in genes of the alcohol dehydrogenase, glutathione S-transferase, and nicotinamide adenine dinucleotide, reduced (NADH) ubiquinone oxidoreductase families
AU Iida, Aritoshi; Saito, Susumu; Sekine, Akihiro; Kitamoto, Takuya; Kitamura, Yuri; Mishima, Chihiro; Osawa, Saori; Kondo, Kimie; Harigae, Satoko; Nakamura, Yusuke
CS Laboratory for Genotyping, The SNP Research Center, Institute of Physical and Chemical Research (RIKEN), Tokyo, Japan
SO Journal of Human Genetics (2001), 46(7), 385-407
CODEN: JHGEFR; ISSN: 1434-5161
PB Springer-Verlag Tokyo
DT Journal
LA English
AB An approach based on development of a large archive of single-nucleotide polymorphisms (SNPs) throughout the human genome is expected to facilitate large-scale studies to identify genes assocd. with drug efficacy and side effects, or susceptibility to common diseases. We have already described collections of SNPs present among various genes encoding drug-metabolizing

enzymes. Here we report SNPs for such enzymes at addnl. loci, including 8 alc. dehydrogenases, 12 glutathione S-transferases, and 18 belonging to the NADH-ubiquinone oxidoreductase family. Among DNA samples from 48 Japanese volunteers, we identified a total of 434 SNPs at these 38 loci: 27 within coding elements, 52 in 5' flanking regions, five in 5' untranslated regions, 293 in introns, 20 in 3' untranslated regions, and 37 in 3' flanking regions. The ratio of transitions to transversions was approx. 2.1 to 1. Among the 27 coding SNPs, 13 were nonsynonymous changes that resulted in amino acid substitutions. Our collection of SNPs derived from this study should prove useful for investigations designed to detect assocns. between genetic variations and common diseases or responsiveness to drug therapy.

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 2000:859191 CAPLUS
DN 135:87750
TI A First High-Density Map of 981 Biallelic Markers on Human Chromosome 14
AU Escary, Jean-Louis; Bottius, Emmanuel; Prince, Nathalie; Reyes, Cecile; Fiawoumo, Yao; Caloustian, Christophe; Bruls, Thomas; Fujiyama, Asao; Cooper, Richard S.; Adeyemo, Adebowale A.; Lathrop, G. Mark; Weissenbach, Jean; Gyapay, Gabor; Foglio, Mario; Beckmann, Jacques S.
CS Centre National de Genotypage, Evry, 91057, Fr.
SO Genomics (2000), 70(2), 153-164
CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB As the largest set of sequence variants, single-nucleotide polymorphisms (SNPs) constitute powerful assets for mapping genes and mutations related to common diseases and for pharmacogenetic studies. A major goal in human genetics is to establish a high-d. map of the genome contg. several hundred thousand SNPs. Here we assayed 3.7 Mb (154,397 bp in 24 alleles) of chromosome 14 expressed sequence tags (ESTs) and sequence-tagged sites, for sequence variation in DNA samples from 12 African individuals. We identified and mapped 480 biallelic markers (459 SNPs and 21 small insertions and deletions), equally distributed between EST and non-EST classes. Extensive research in public databases also yielded 604 chromosome 14 SNPs (dbSNPs), 520 of which could be mapped and 19 of which are common between CNG (i.e., identified at the Center National de Genotypage) and dbSNP polymorphisms. We present a dense map of SNP variation of human chromosome 14 based on 981 nonredundant biallelic markers present among 1345 radiation hybrid mapped sequence objects. Next, bioinformatic tools allowed 945 significant sequence alignments to chromosome 14 contigs, giving the precise chromosome sequence position for 70% of the mapped sequences and SNPs. In addn., these tools also permitted the identification and mapping of 273 SNPs in 159 known genes. The availability of this SNP map will permit a wide range of genetic studies on a complete chromosome. The recognition of 45 genes with multiple SNPs, by allowing the construction of haplotypes, should facilitate pharmacogenetic studies in the corresponding regions. (c) 2000 Academic Press.

RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	35.51	35.72

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-5.21	-5.21

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